

5994513

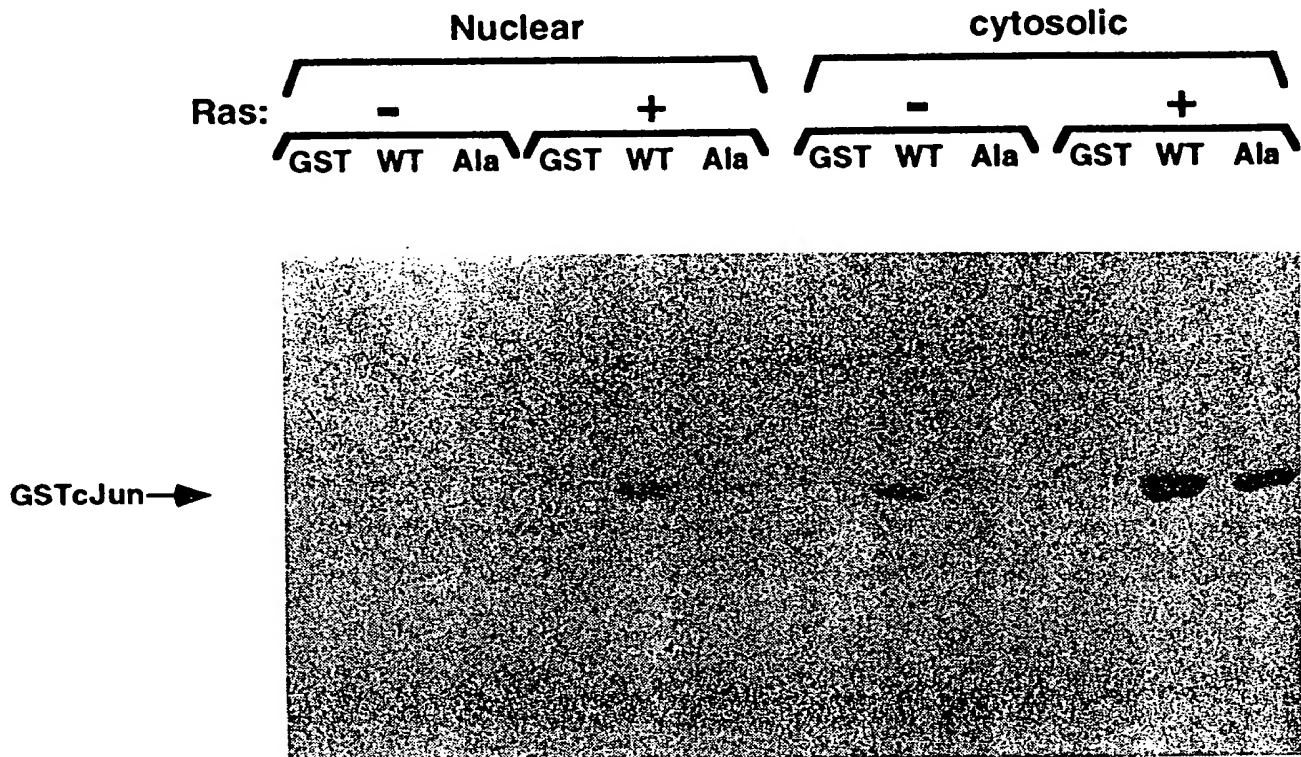


FIG. I

Treatment:	-	TPA	TPA	TPA	TPA
Substrate:	WT	WT	WT	WT	Ala
Time:	0	10	30	30	30

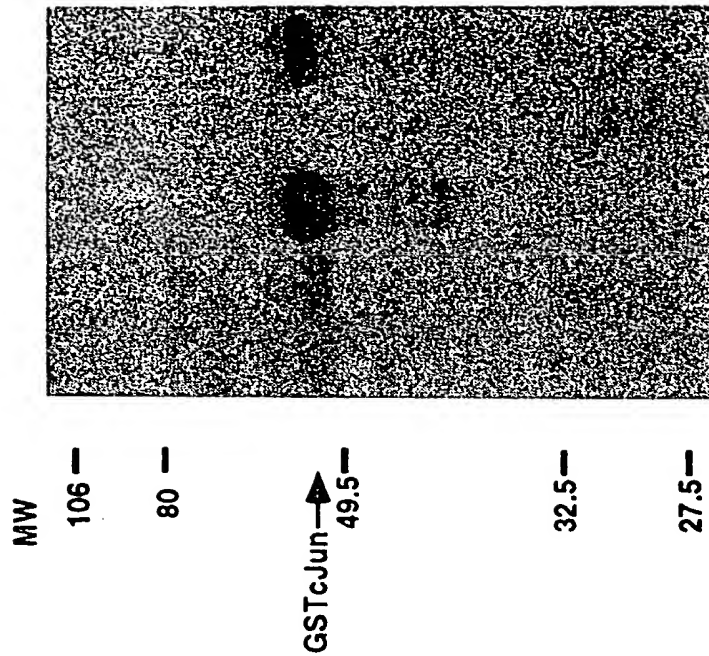


FIG. 2A

Treatment:	-	UV	UV	UV	TPA	TPA
Substrate:	WT	WT	WT	Ala	WT	WT
Time:	0	5	30	30	5	30

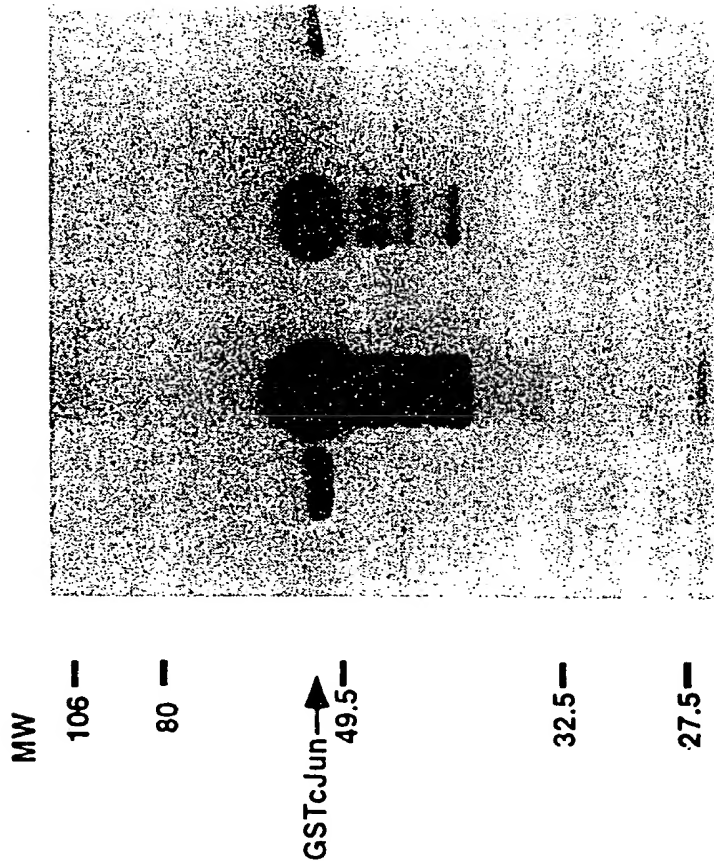


FIG. 2B

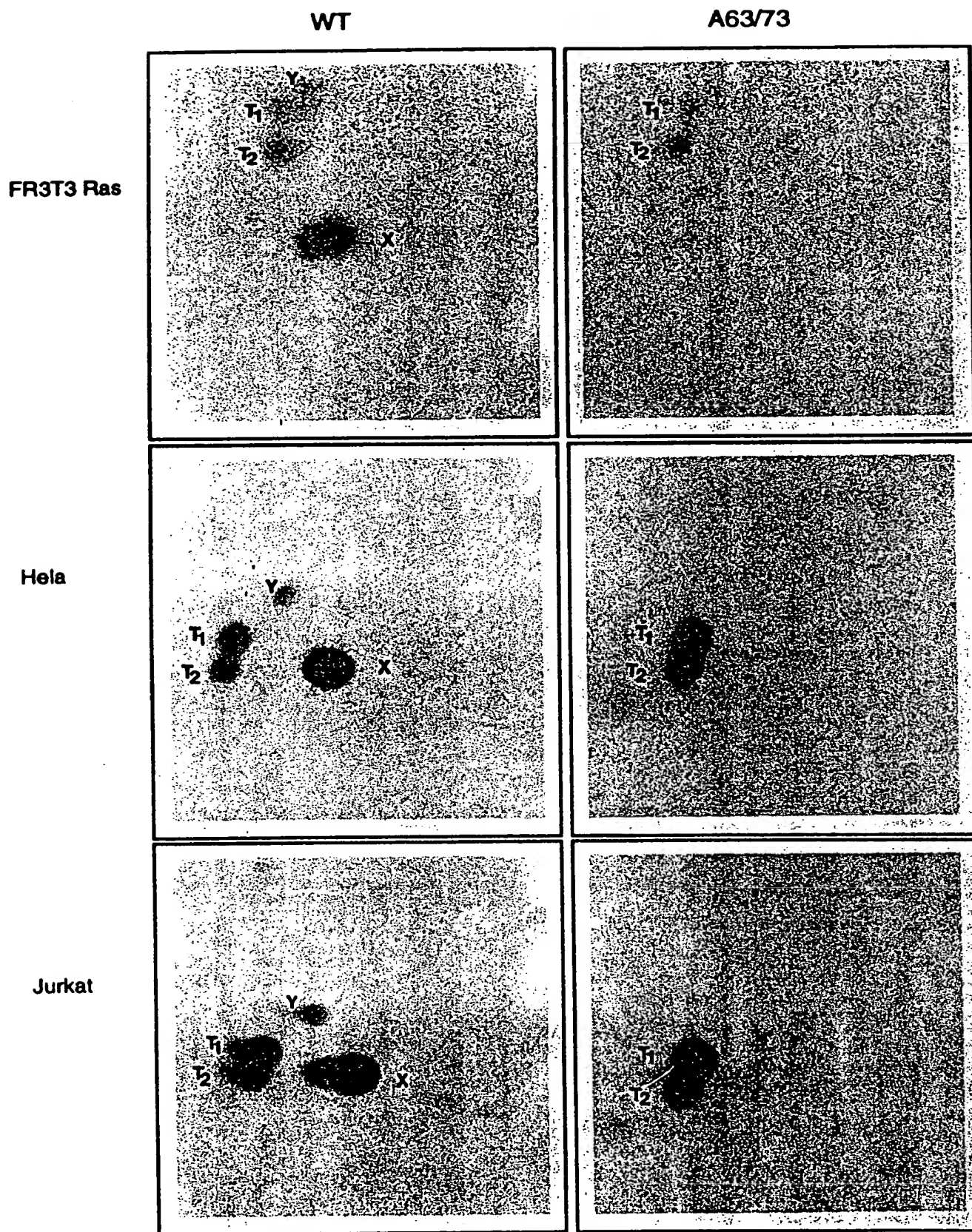
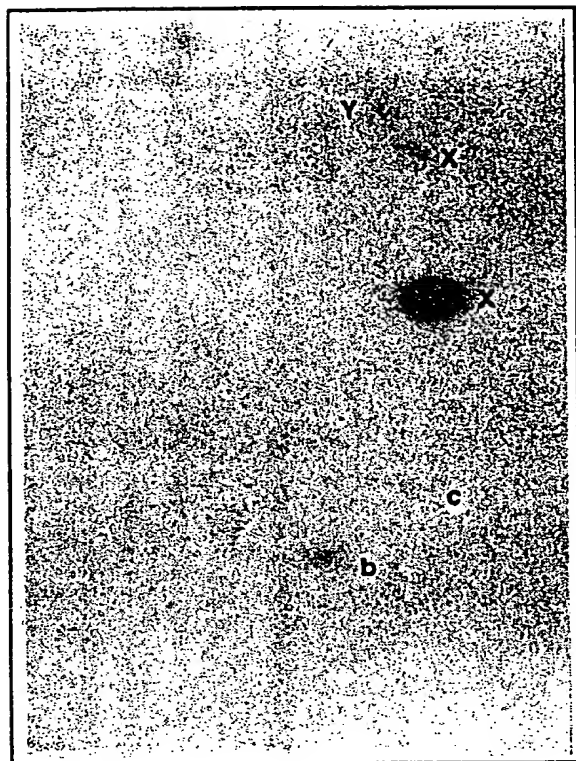


FIG. 3A

In Vitro



In Vivo

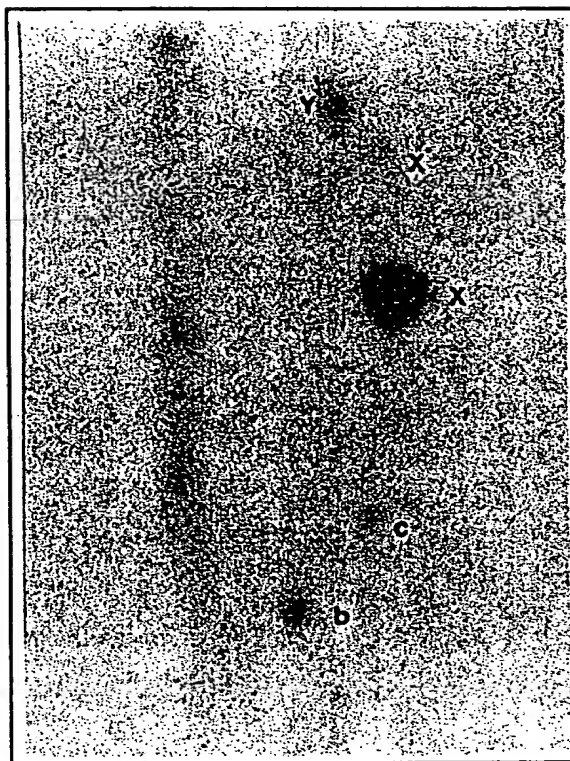


FIG. 3B

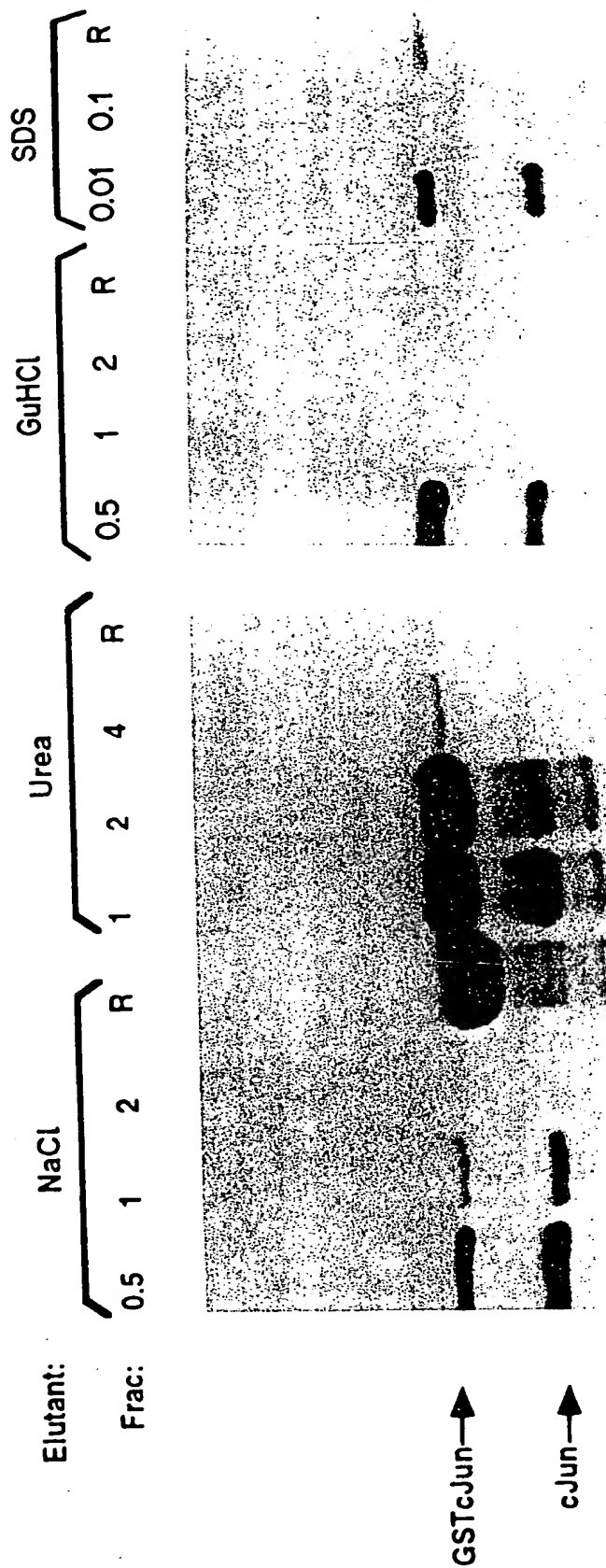


FIG. 4A

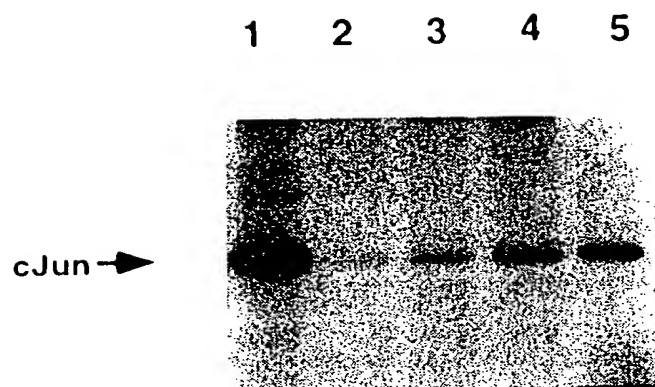


FIG. 4B

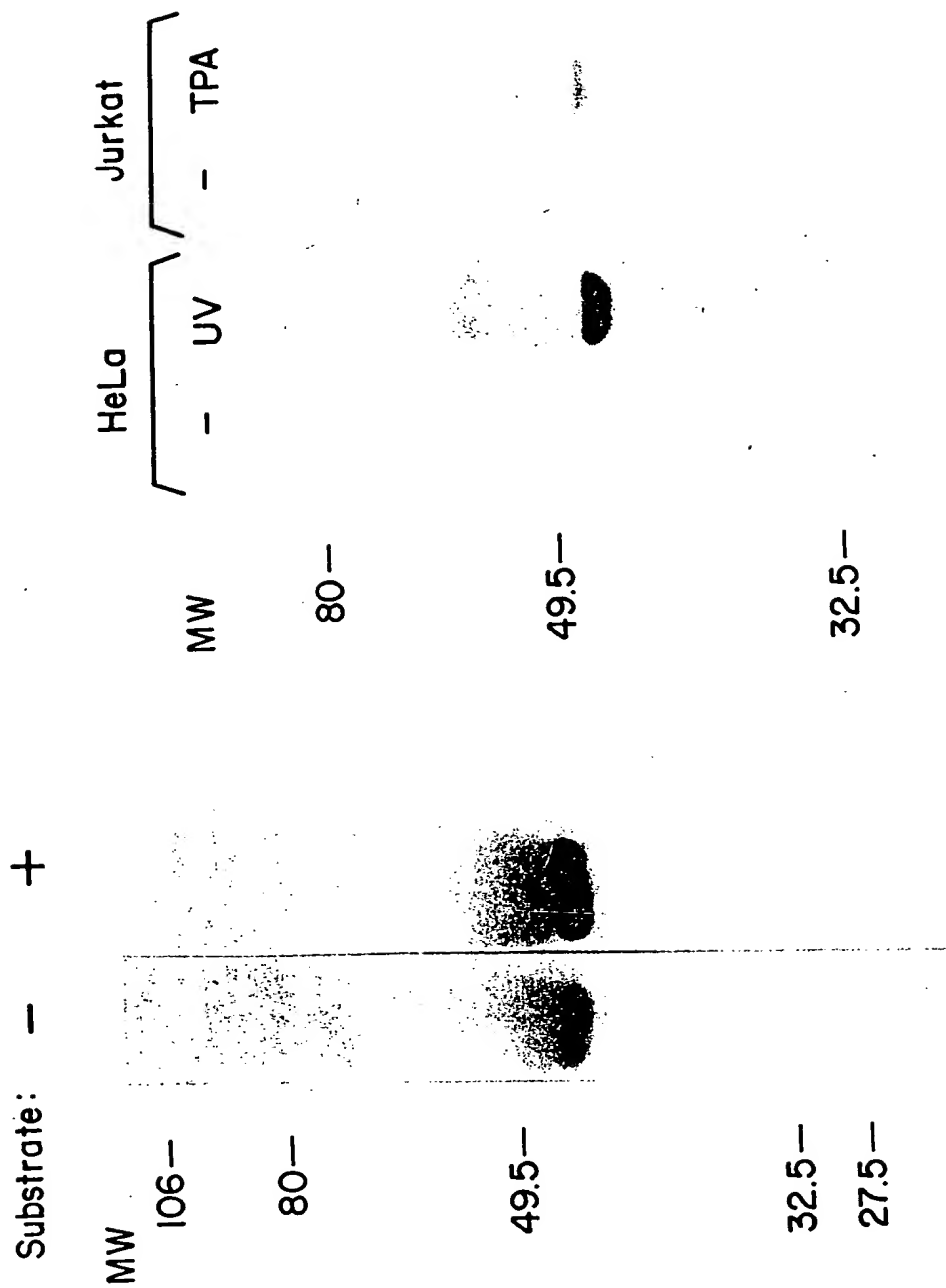
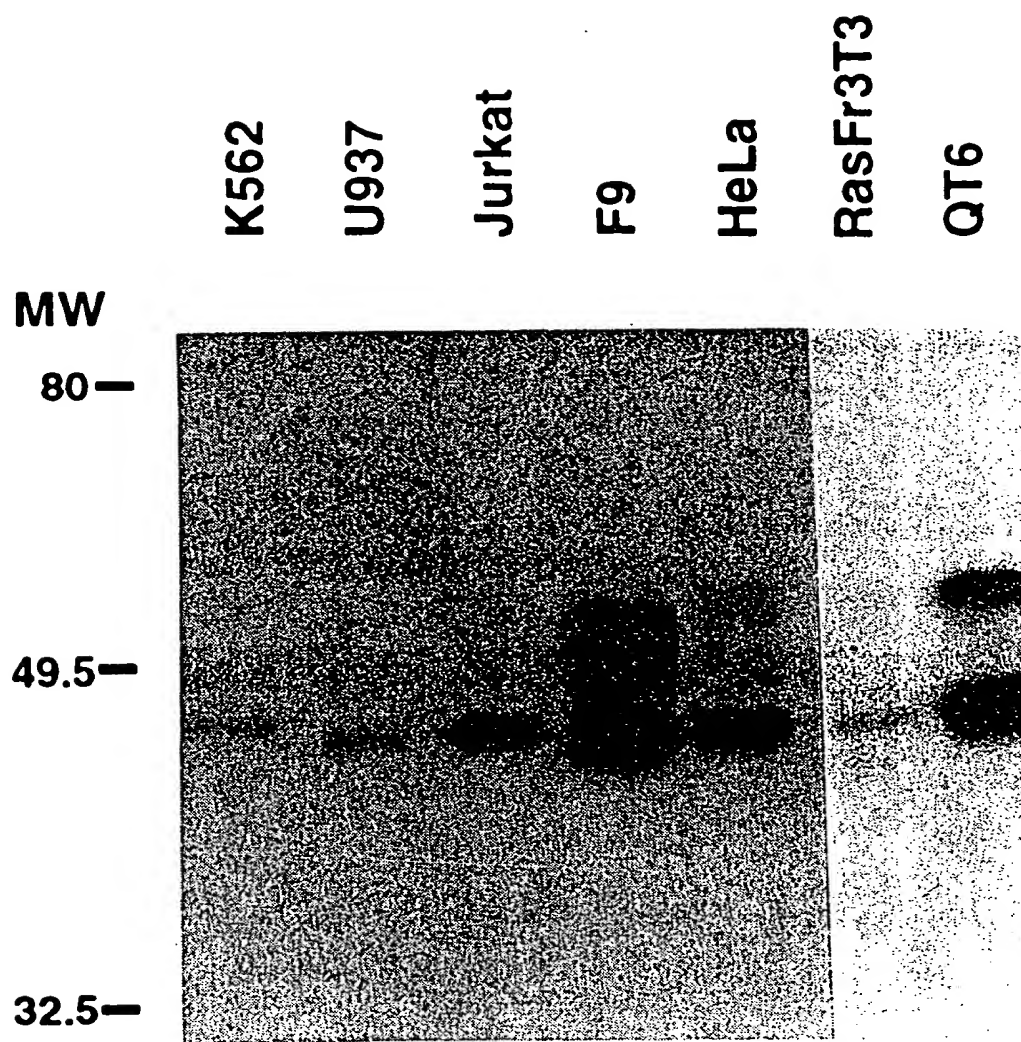


FIG. 5B

FIG. 5A

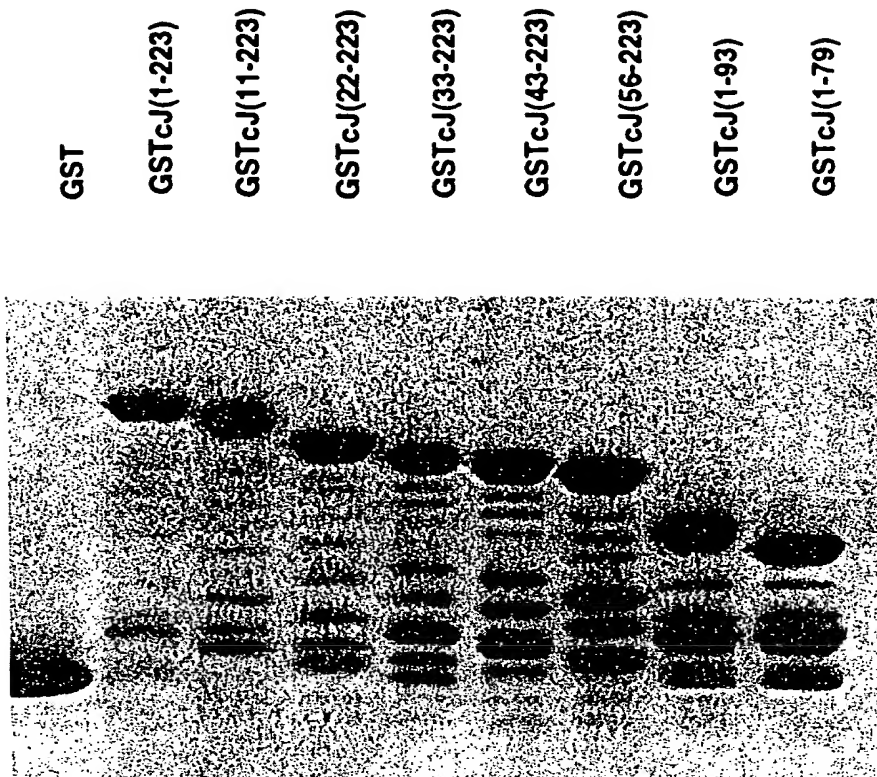


**FIG. 5C**



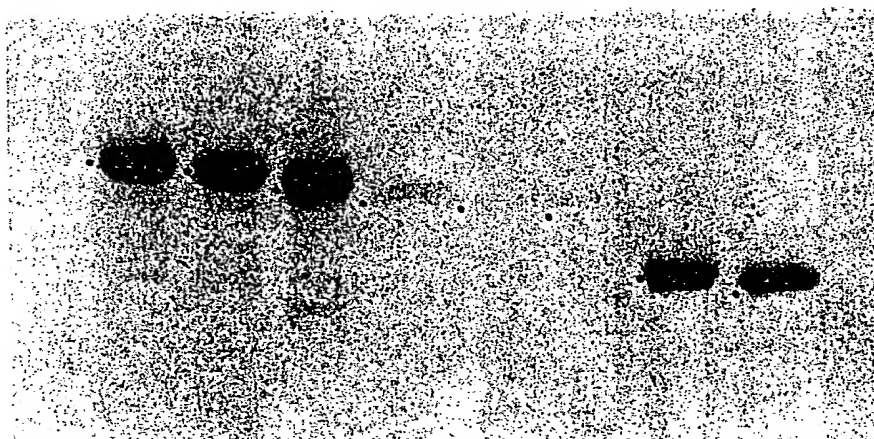
Protein Gel

FIG.6A



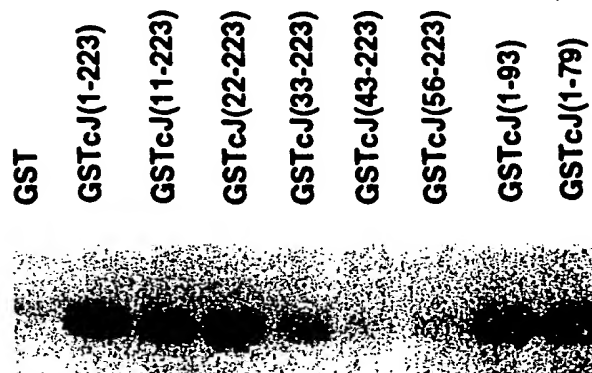
<sup>32</sup>P-Immobilized Substrate

FIG.6B



<sup>32</sup>P-Exogenous Substrate

FIG.6C



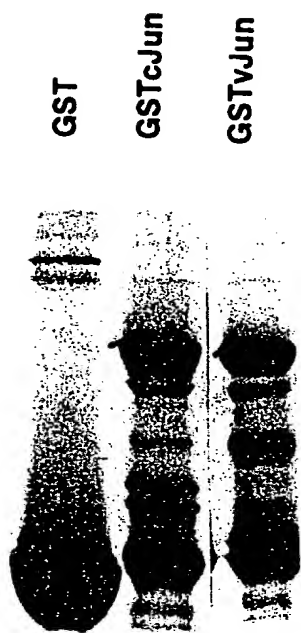


FIG. 7A

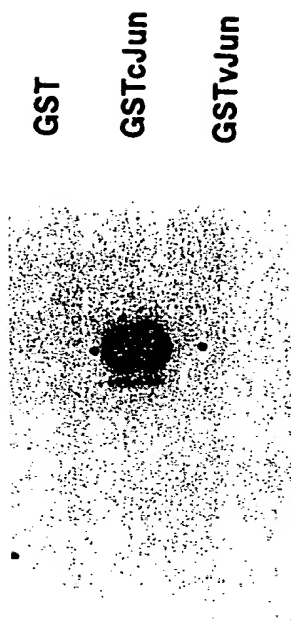


FIG. 7B



FIG. 7C

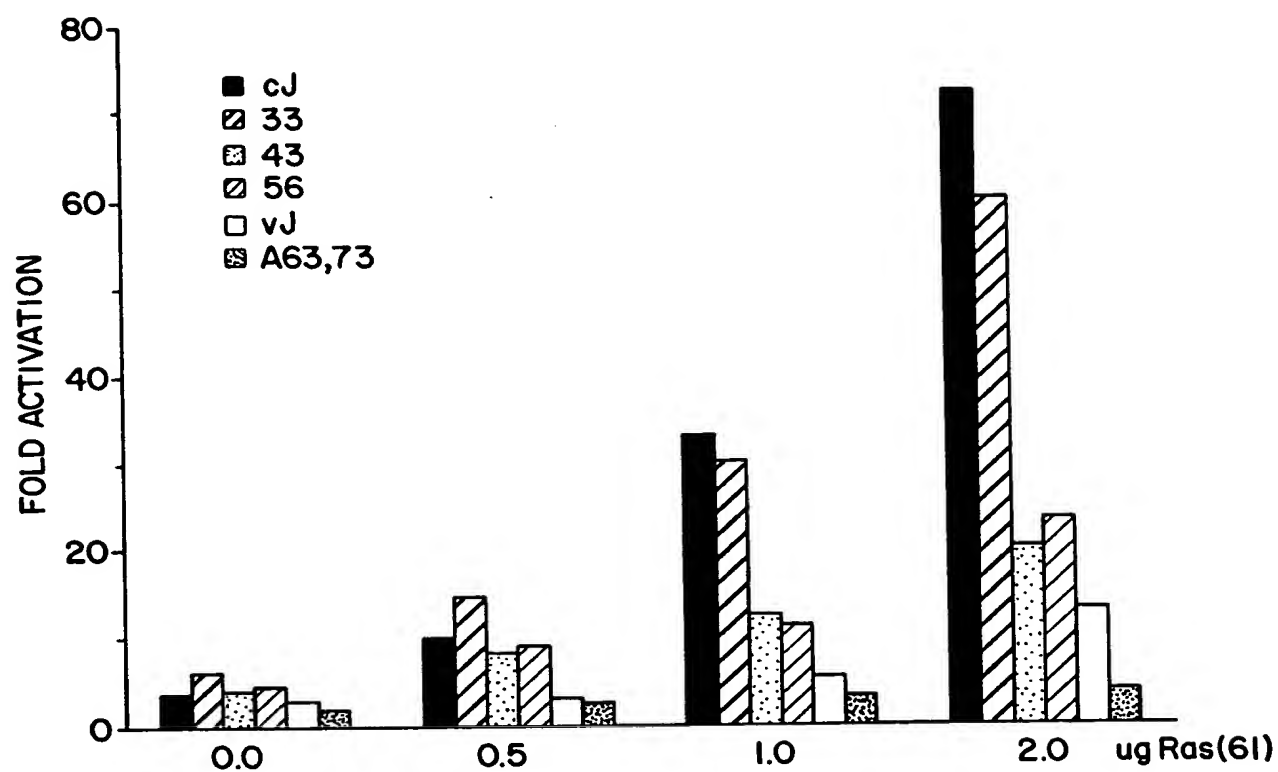


FIG. 8A

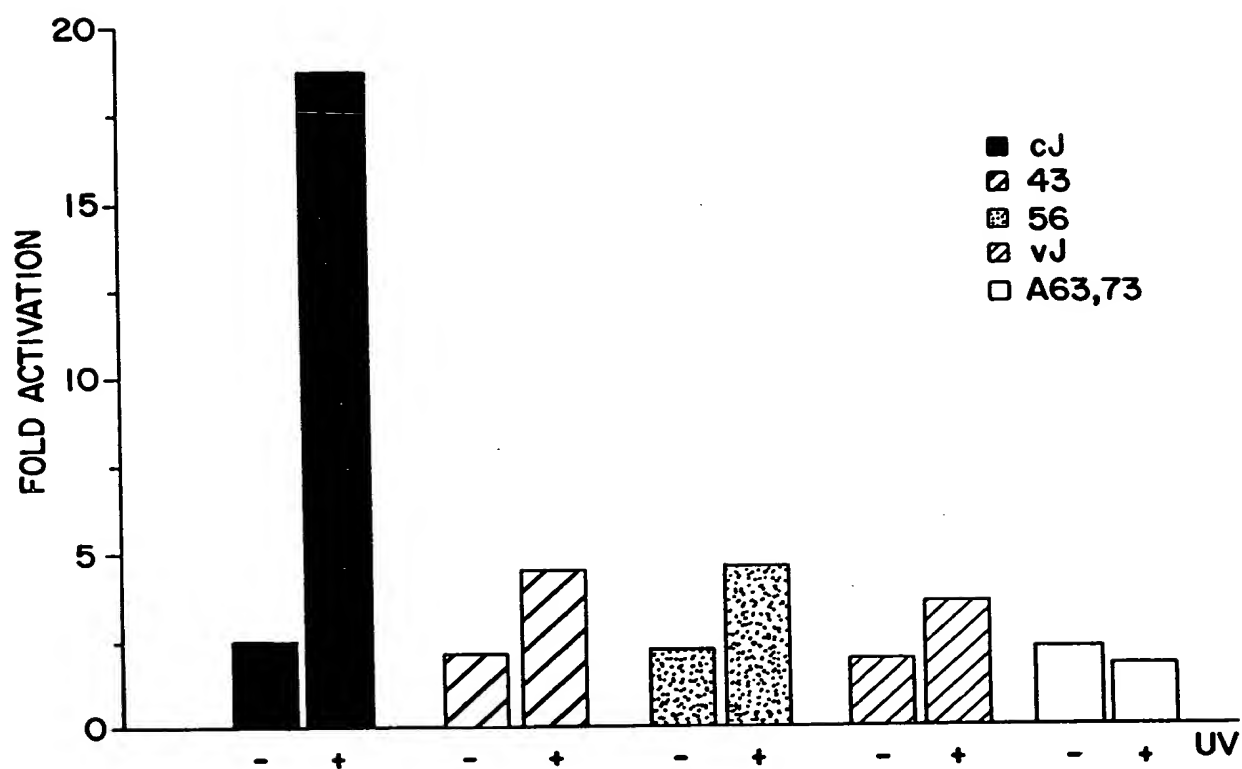


FIG. 8B

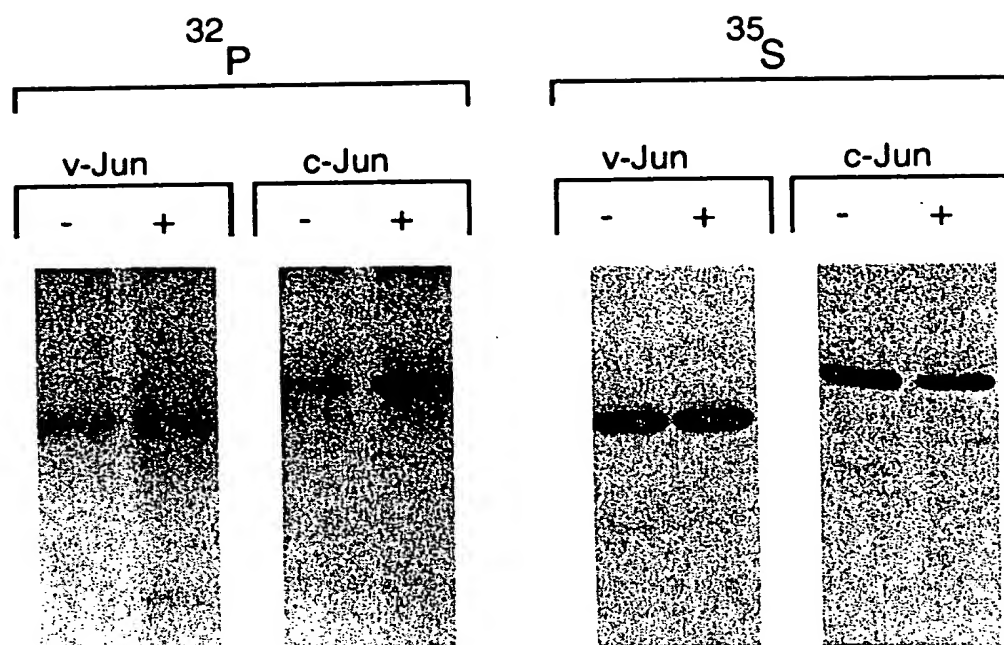


FIG. 9A

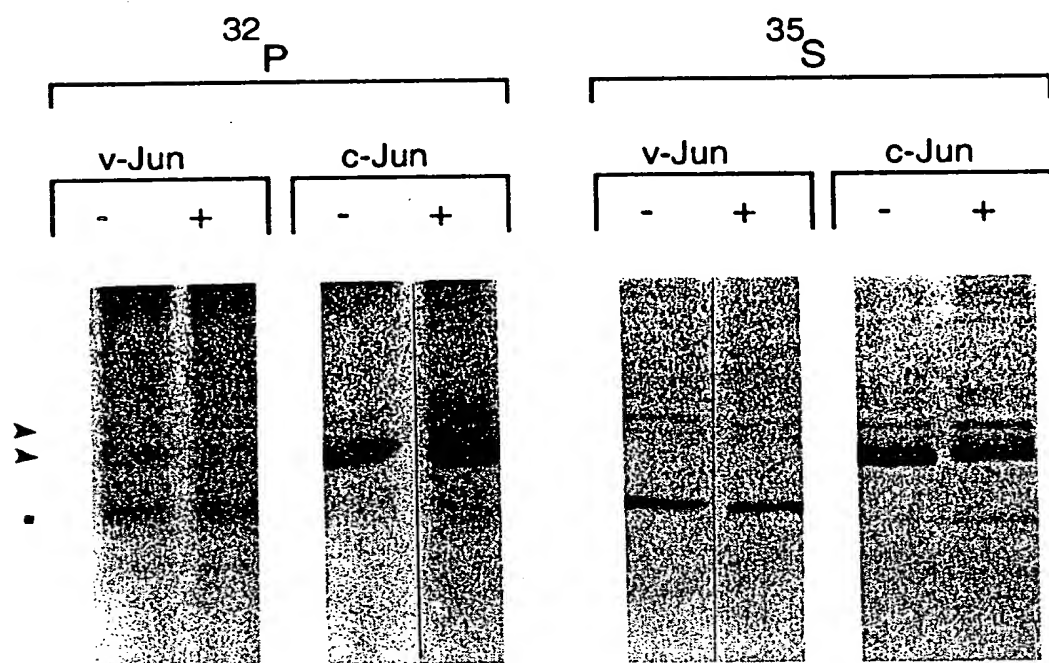


FIG. 9B

GAATTCCGGG	GGGGCCAAGA	CCCGCCGCCG	GCCGGCCACT	GCAGGGTCCG	CACTGATCCG	60
CTCCGGCGGA	GAGCCGCTGC	TCTGGGAAGT	CAGTTCGCCT	GCGGACTCCG	AGGAACGGCT	120
GCGCACGAAG	AGCCGTCAGT	GAGTGACCGC	GACTTTTCAA	AGCCGGGTAG	GGCGCGCGAG	180
TCGACAAGTA	AGAGTGCGGG	AGGCATCTTA	ATTAACCCCTG	CGCTCCCTGG	AGCAGCTGGT	240
GAGGAGGGCG	CACGGGGACG	ACAGCCAGCG	GGTGCGTGCG	CTCTTAGAGA	AACTTTCCCT	300
GTCAAAGGCT	CCGGGGGGCG	CGGGTGTCCT	CCGCTTGCCA	CAGCCCTGTT	GCGGCCCCGA	360
AACTTGTCGG	CGCACGCCAA	ACTAACCTCA	CGTGAAGTGA	CGGACTGTTC	T ATG ACT	417
					Met Thr	
					1	
GCA AAG ATG	GAA ACG ACC	TTC TAT GAC	GAT GCC CTC	AAC GCC TCG	TTC	465
Ala Lys Met	Glu Thr Thr Phe	Tyr Asp Asp	Ala Leu Asn	Ala Ser Phe		
		5	10	15		
CTC CCC TCC	GAG AGG GGA	CCT TAT GGC	TAC AGT AAC	CCC AAG ATC	CTG	513
Leu Pro Ser	Glu Arg Gly	Pro Tyr Gly	Tyr Ser Asn	Pro Lys Ile	Leu	
		20	25	30		
AAA CAG AGC	ATG ACC CTG	AAC CTG GCC	GAC CCA GTG	GGG AGC CTG	AAG	561
Lys Gln Ser	Met Thr Leu	Asn Leu Ala	Asp Pro Val	Gly Ser Leu	Lys	
		35	40	45	50	

FIG.10A

CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC GTG	609
Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val	65
GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC ATA ATC CAG	657
Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln	80
TCC AGC AAC GGG CAC ATC ACC ACC ACC CCG ACC ACC CAG TTC CTG	705
Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Thr Gln Phe Leu	95
TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC TTC	753
Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe	110
GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC AGC CTG CCC AGC GTG	801
Val Arg Ala Leu Ala Glu Leu His Ser Ser Gln Asn Thr Leu Pro Ser Val	125
ACG TCG GCG GCG CAG CCG GTC AAC GCG GCA GGC ATG GTG GCT CCC GCG	849
Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala	145
GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC TTC AGC GCC AGC	897
Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser	160

FIG.10B

CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC CCA	945
Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn Pro	
165 170 175	
GGC GCG CTG AGC AGC GGC GGC GGC GGC TCC TAC GGC GCG GCC GGC	993
Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala Gly	
180 185 190	
CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CCG CCG CAC CAC CAC	1041
Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Pro Pro His His	
195 200 205 210	
CTG CCC CAG CAG ATG CCC GTG CAG CAG CAG CCG CTG CAG GCC CTG AAG	1089
Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Ala Leu Lys	
215 220 225	
GAG GAG CCT CAG ATA GTG CCC GAG ATG CCC GGC GAG ACA CCG CCC CTG	1137
Glu Glu Pro Gln Ile Val Pro Glu Met Pro Gly Glu Thr Pro Pro Leu	
230 235 240	
TCC CCC ATC GAG ATG GAG TCC CAG GAG CCG ATC AAG GCG GAG AGG AAG	1185
Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg Lys	
245 250 255	
CGC ATG AGG AAC CCG ATC GCT GCC TCG AAG TGC CGA AAA AGG AAG CTG	1233
Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys Leu	
260 265 270	

FIG. 10C

GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT CAG Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln 275 280 285 290	1281
AAC TCG GAG CTG GCG TCG ACG GCC AAC ATG CTC AGG GAA CAG GTC GCA Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala 295 300 305	1329
CAG CTT AAA CAC AAA GTC ATG AAC CAC GTT AAC AGT GGG TGC CAA CTC Gln Leu Lys His Lys Val Met Asn His Val Asn Ser Gly Cys Gln Leu 310 315 320	1377
ATC CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGGGG Ile Leu Thr Gln Gln Leu Gln Thr Phe 325 330	1424
CTGAGGGGCA ACGAAGAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT	1484
GCGACGGAGA GAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG	1544
GGTTCCGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA CCACCTGGTC GCGCCCTCCC	1604
TTGGCGTCGA GCCAGGGAGC GCGCGCCTGG GGGCTGCCCC GCTTTGCGGA CGGGCTGTCC	1664
CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA	1724

FIG.10D



TTCGATCTCA	TTCAGTATTA	AAGGGGCAG	GGGAGGGG	TTACAAACTG	CAATAGAGAC	1784
TGTAGATTGC	TTCTGTAAGTA	CTCCTTAAGA	ACACAAAGCG	GGGGAGGGT	TGGGAGGGG	1844
CGGCAGGAGG	GAGGTTTGTG	AGAGCGAGGC	TGAGCCTACA	GATGAACTCT	TTCTGGCCTG	1904
CTTTCGTAA	CTGTGTATGT	ACATATATAT	ATTTTTTAAAT	TTGATTAAAG	CTGATTACTG	1964
TCAATAAACA	GCTTCATGCC	TTTGTAAGTT	ATTTCCTGTT	TGTTTGTTTG	GGATCCTGCC	2024
CAGTGTGTT	TGTAAATAAG	AGATTGGAG	CACTCTGAGT	TTACCATTTG	TAATAAAGTA	2084
TATAATTTT	TT					2096

FIG. 10E

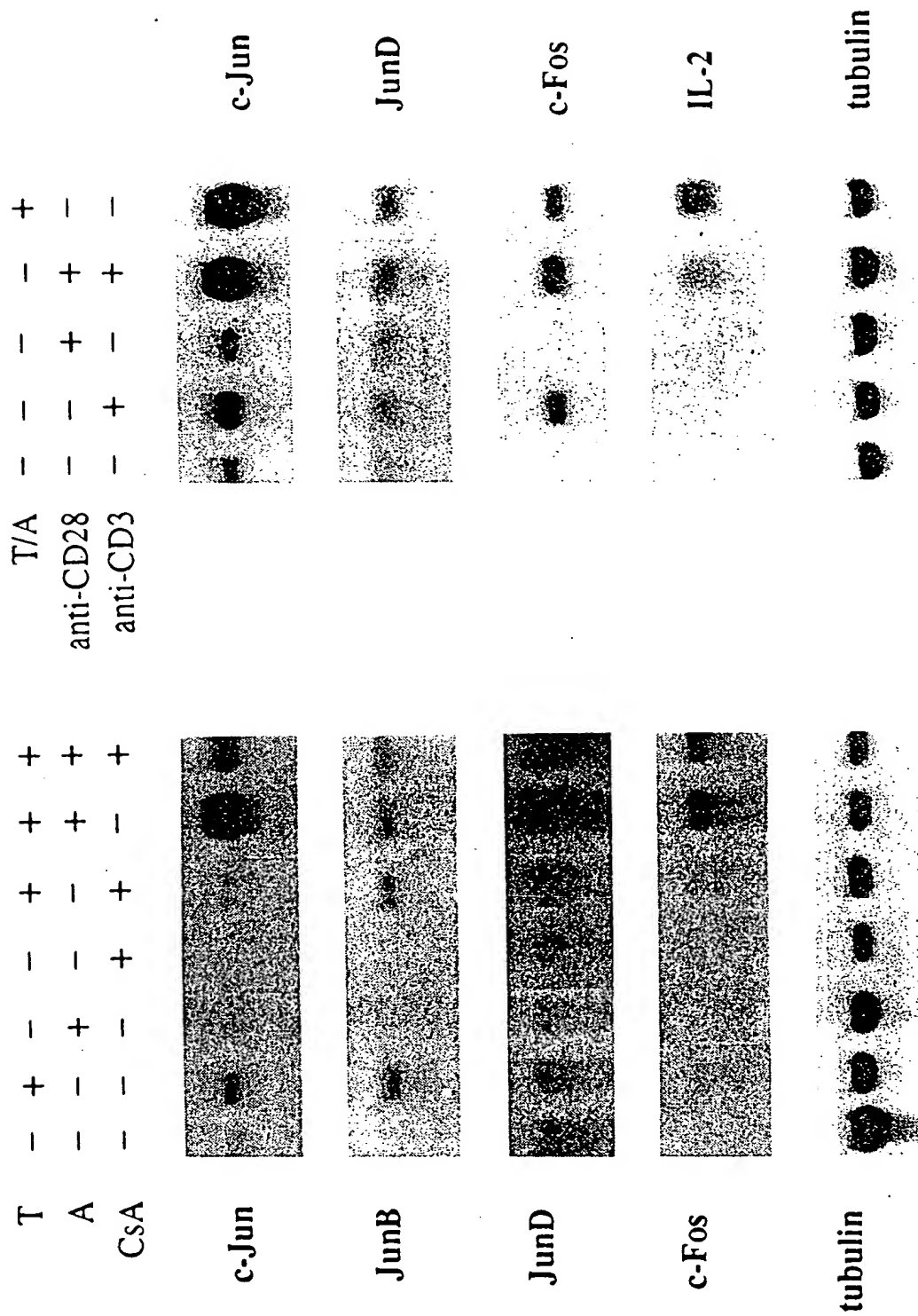


FIG.11A

FIG.11B

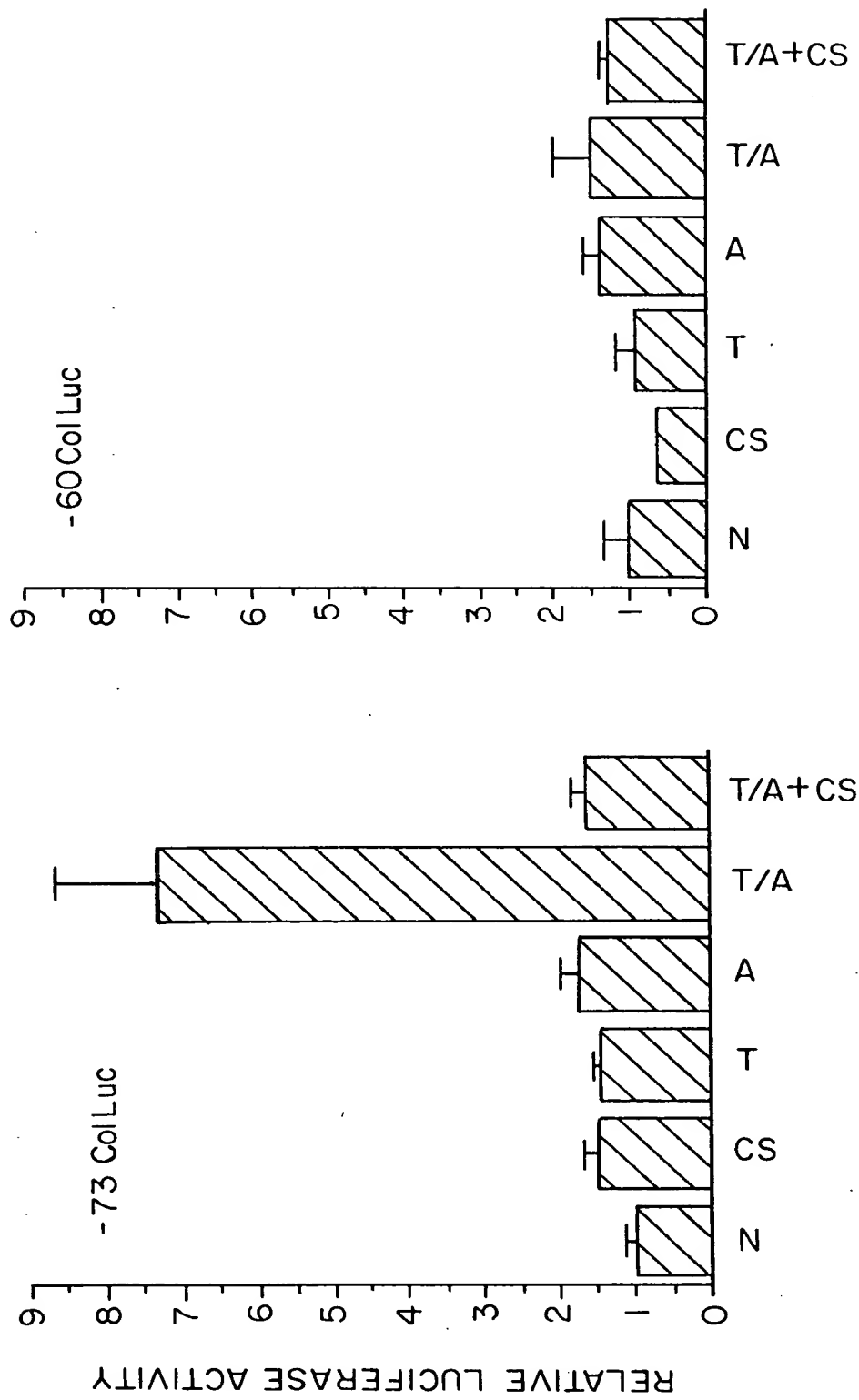


FIG. 11C

FIG.12A

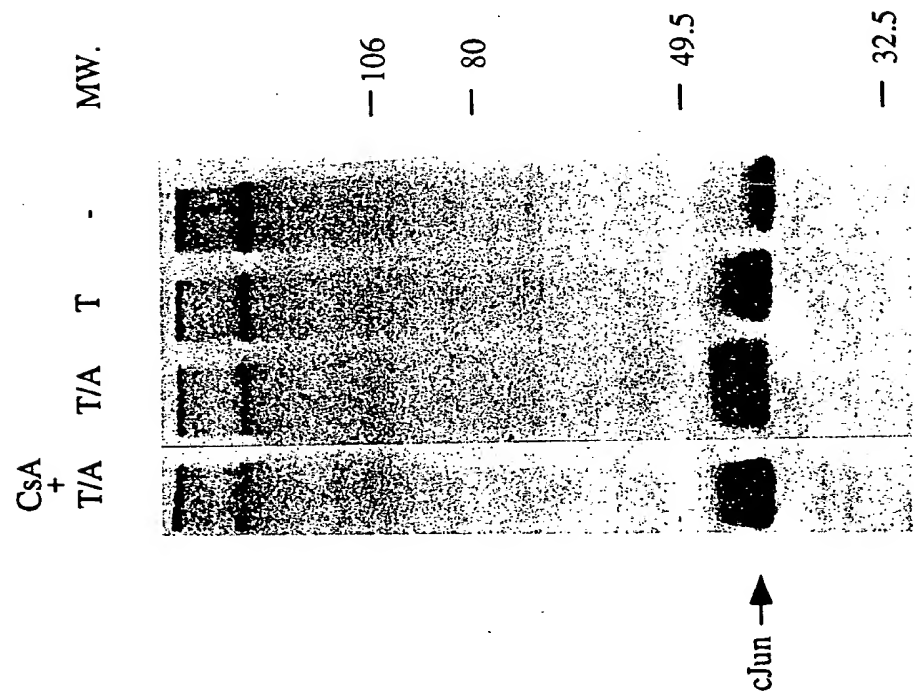
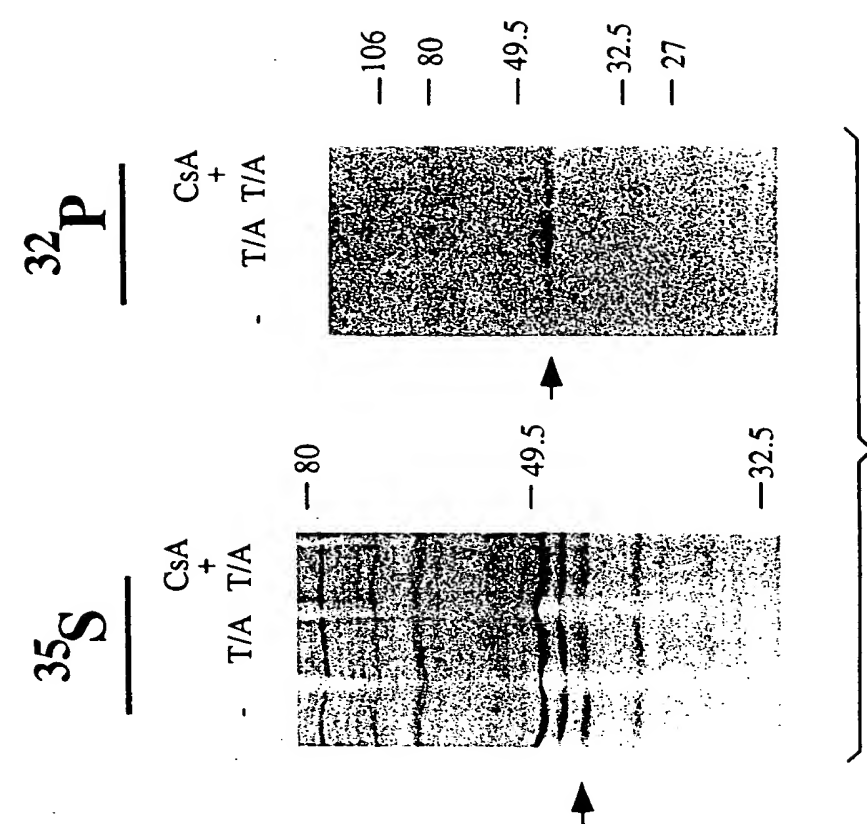


FIG.12B



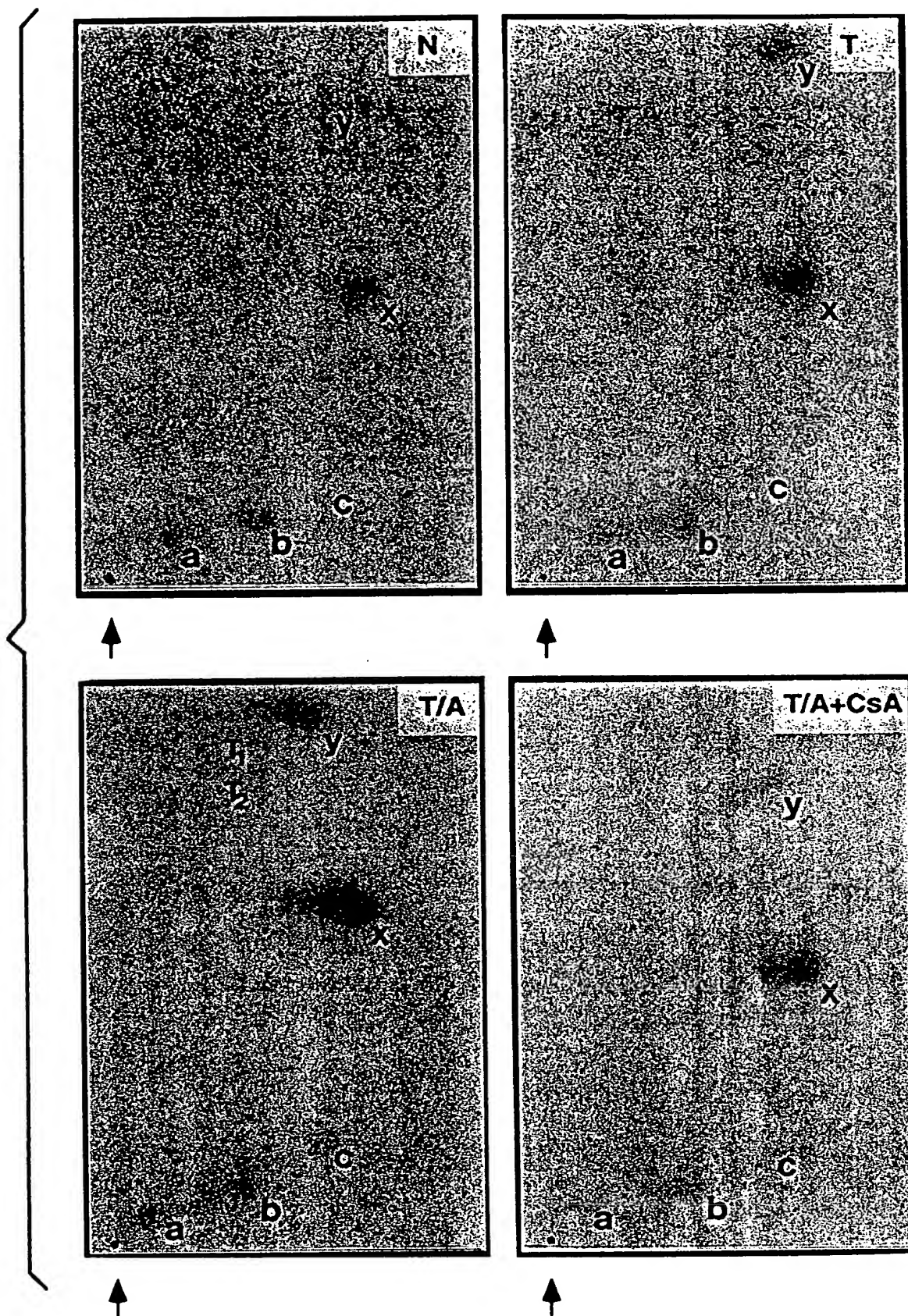


FIG.12C

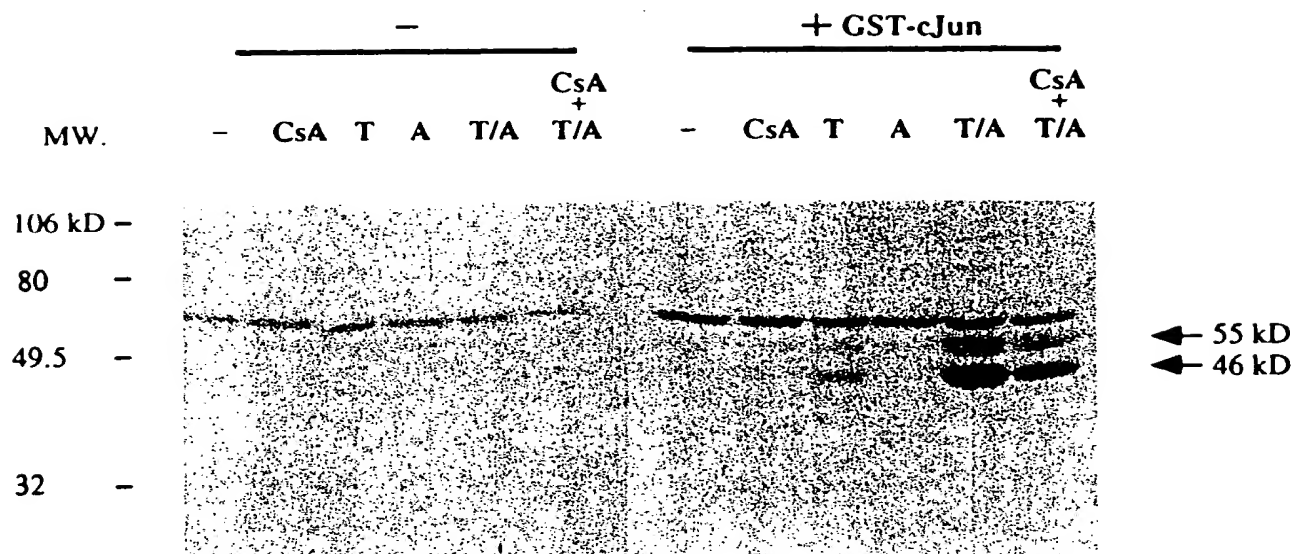


FIG.13A

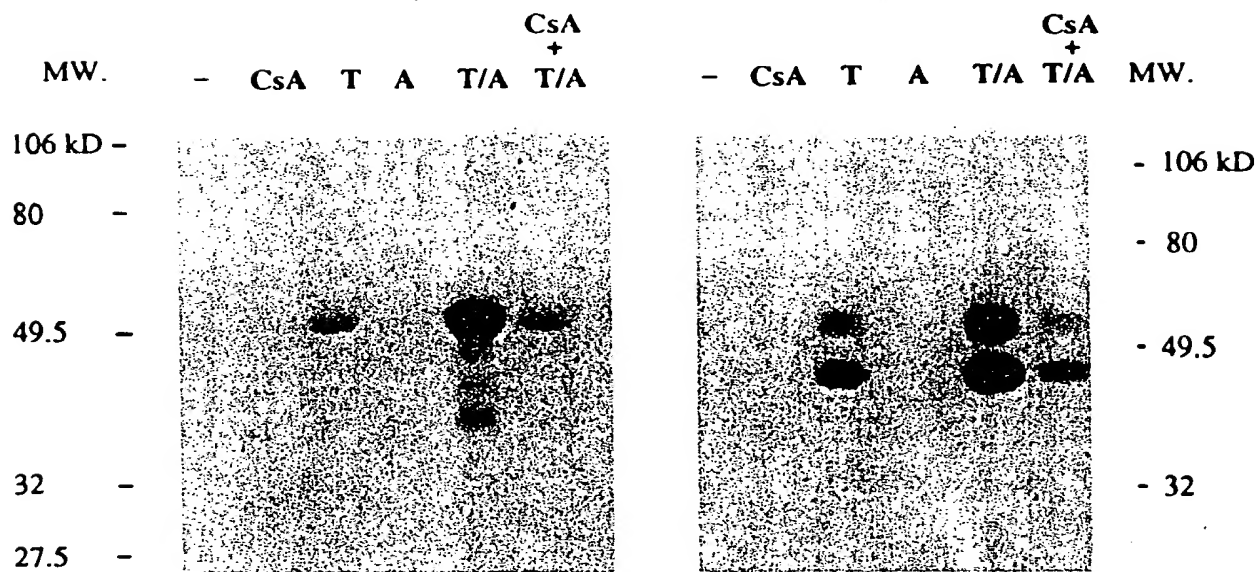


FIG.13B

FIG.13C

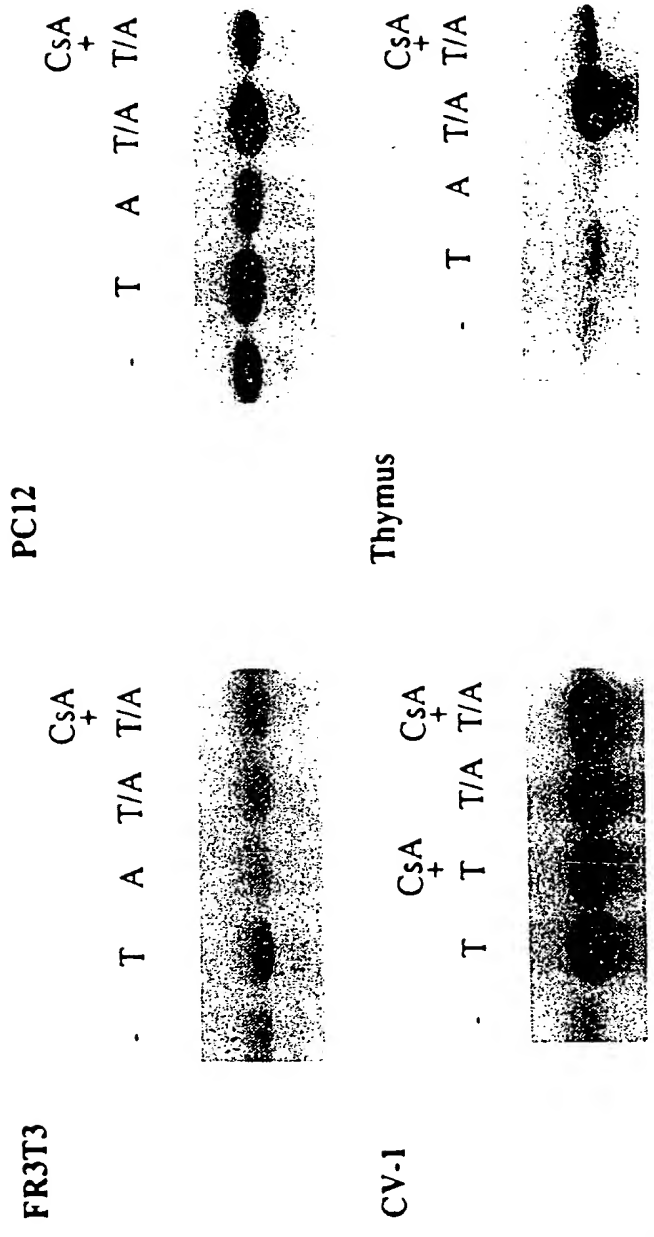


FIG.14

FIG.15A

Erk-1 Mut →

- CsA T A T/A T/A

CsA  
+

MW.

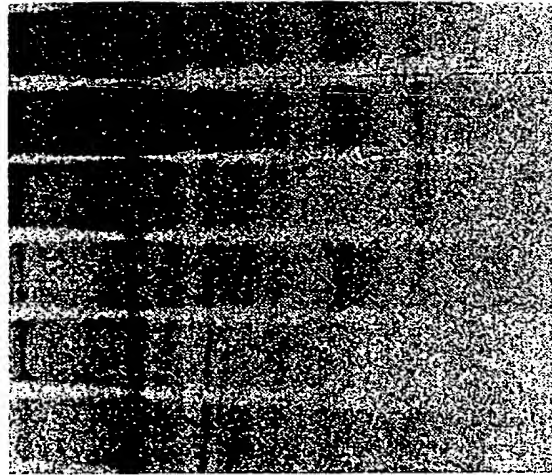


FIG.15C

Erk-1 Mut →

- T A T/A T/A

CsA  
+

MW.

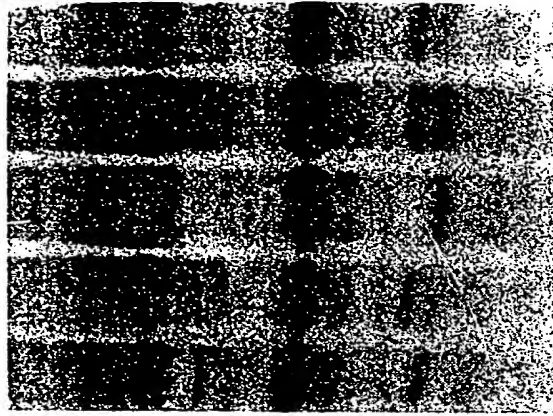


FIG.15B

MBP →



FIG.15D

MBP →





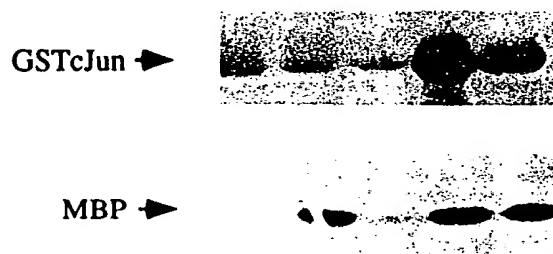
# FIG.16A

CsA	+	-	-	-	-
anti-CD28	+	+	-	+	-
anti-CD3	+	+	+	-	-



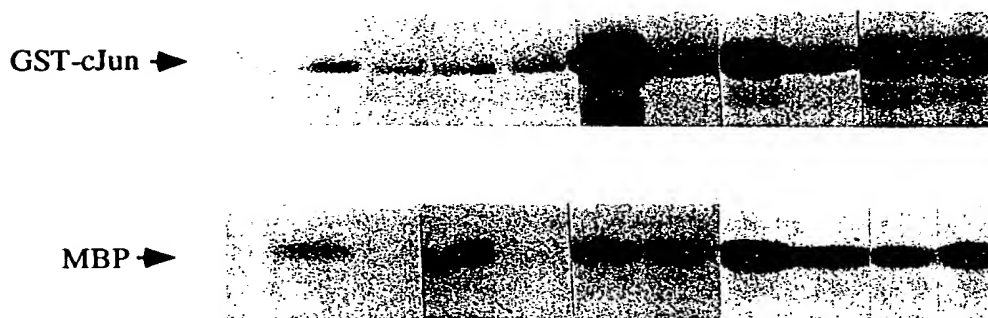
# FIG.16B

CsA	-	-	-	-	+
anti-CD28	-	-	+	+	+
anti-CD3	-	+	-	+	+



# FIG.16C

	1	2	3	4	5	6	7	8	9	10	11
CsA	-	-	-	-	-	-	+	-	+	-	+
anti-CD28	-	-	-	-	+	-	-	-	-	+	+
anti-CD3	-	-	-	+	-	-	-	+	+	-	-
A	-	-	+	-	-	+	+	-	-	-	-
T	-	+	-	-	-	+	+	+	+	+	+



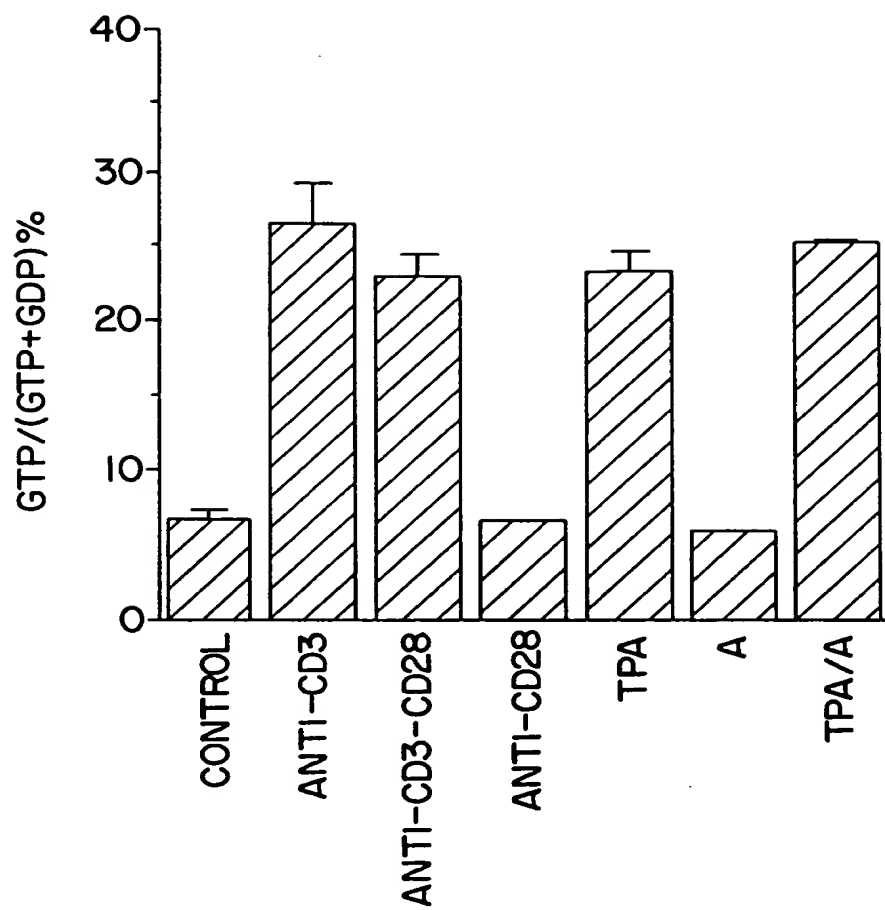


FIG. 17A

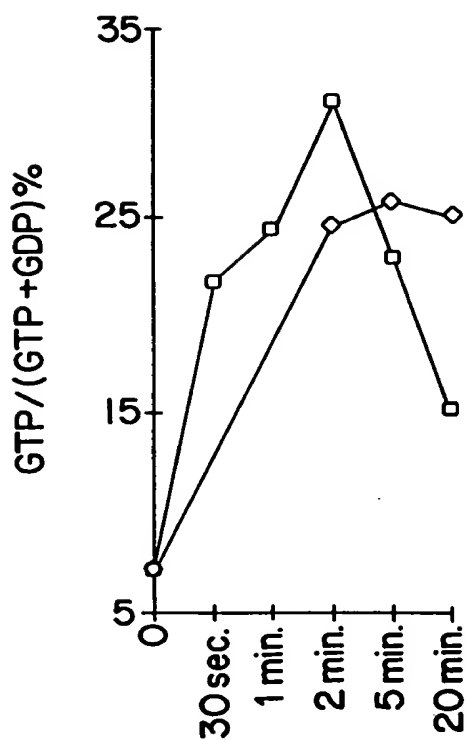


FIG. 17B